

- 1 -

SEQUENCE LISTING

<110> Hepgenics Pty Ltd

<120> Viral Vector

<130> 12437050/EJH

<150> AU 2003901876

<151> 2003-04-17

<160> 13

<170> PatentIn version 3.0

<210> 1

<211> 25

<212> DNA

<213> duck

<400> 1

gggcaacatc cagcaaaatc aatgg

25

<210> 2

<211> 30

<212> DNA

<213> human

<400> 2

gctgcggaat ggctaaaagg gcccccgacc

30

- 2 -

<210> 3

<211> 34

<212> DNA

<213> human

<400> 3

ccaacactag atcacgaaac ccacgtcacc gggg

34

<210> 4

<211> 34

<212> DNA

<213> human

<400> 4

ggttgatgac tagtgctttg ggtgcagtgg cccc

34

<210> 5

<211> 3021

<212> DNA

<213> duck

<400> 5

catgctcatt tgaaagctta tgcaaaaatt aacgaggaat cactggatag ggctaggaga	60
ttgcttttggg ggcattacaa ctgtttactg tggggagaag ctcaagttac taactatatt	120
tctcgtttgc gtacttggtt gtcaactcct gagaaatata gaggtagaga tgccccgacc	180
attgaagcaa tcactagacc aatccaggtg gtcagggag gcagaaaaac aactacgggt	240
actagaaaac ctctgtggact cgaacctaga agaagaaaag ttaaaaccac agttgtctat	300
gggagaagac gttcaaagtc ccgggaaagg agagccccta caccccaacg tgcgggctcc	360
cctctccac gtagttcgag cagccaccat agatctccct cgctaggaa ataaattacc	420
tgctaggcat cacttaggta aattgtcagg actatatcaa atgaagggt gtacttttaa	480
cccagaatgg aaagtaccag atatttcgga tactcatttt aatttagatg tagttaatga	540

- 3 -

gtgcccttcc	cgaaattgga	aatatttgac	tccagccaaa	ttctggccca	agagcatttc	600
ctactttcct	gtccaggtag	gggttaaacc	aaagtatcct	gacaatgtga	tgcaacatga	660
atcaatagta	ggtaaattatt	taaccaggct	ctatgaagca	ggaatccttt	ataagcggat	720
atctaaacat	ttggtcacat	ttaaagggtca	gccttataat	tggaacagc	aacaccttgt	780
caatcaacat	cacatttatg	atggggcaac	atccagcaaa	atcaatggac	gtcagacgga	840
tagaaggagg	agaaatactg	ttaaaccaac	ttgccggaag	gatgatccca	aaagggactt	900
tgacatggtc	aggcaagttt	ccaacactag	atcacgtgtt	agaccatgtg	caaacaatgg	960
aggagataaa	caccctccag	aatcaggagg	cttggcctgc	tggggcggga	aggagagtag	1020
gattatcaaa	tccgactcct	caagagattc	ctcagcccca	gtggactccc	gaggaagacc	1080
aaaaagcacg	cgaagctttt	cgccgttata	aagaagaaag	accaccggaa	accaccacca	1140
ttcctccgtc	ttccccctct	cagtgggaagc	tacaaccggg	ggacgatcca	ctcctgggaa	1200
atcagtctct	cctcgagaact	catccgctat	accagtcaga	accagcgggtg	ccagtataaa	1260
aaactcccc	cttgaagaag	aaaatgtctg	gtaccttcgg	gggaataacta	gctggcctaa	1320
tcggattact	ggtaagcttt	ttcttggtga	taaaaattct	agaaatactg	aggaggctag	1380
attggtggtg	gatttctctc	agttctccaa	agggaataat	gcaatgcgct	ttccaagata	1440
ctggagccca	aatctctcca	cattacgtag	gatcttgccc	gtggggatgc	ccaggatttc	1500
tttgaccta	tctcaggctt	tttatcatct	tcctcttaat	cctgctagta	gcagcaggct	1560
tgctgtatct	gacggacaac	gggtctacta	ttttaggaaa	gctccaatgg	gcgtcggctt	1620
cagccctttt	ctcctccatc	tcttcaactac	tgccctcgga	tccgaaatct	ctcgtcgtct	1680
taacgtttgg	actttcactt	atatggatga	cttctctctc	tgccacccaa	acgctcgtca	1740
ccttaacgca	attagccacg	ctgtctgctc	ttttttacaa	gagttaggaa	taagaataaa	1800
ctttgacaaa	accacgcctt	ctccggtgaa	tgaaataaga	ttcctcgggt	accagattga	1860
tgaaaatttc	atgaagattg	aagaaagcag	atggaaagaa	ttaaggactg	taatcaagaa	1920
aataaaagta	ggagaatggt	atgactggaa	atgtattcaa	agatttggtg	ggcatttgaa	1980
ttttgttttg	ccttttacta	aaggtaatat	tgaaatgtta	aaaccaatgt	atgctgctat	2040
tactaaccaa	gtaaacttta	gcttctcttc	atcctatagg	actttgttat	ataaactaac	2100
aatgggtgtg	tgtaaattaa	gaataaagcc	aaagtcctct	gtacctttgc	cacgtgtagc	2160
tacagatgct	acccaacac	atggcgcaat	atcccatatc	accggcggga	gcgcagtgtt	2220

- 4 -

```

tgctttttca aaggtcagag atatacatgt tcaggaacta ttgatgtctt gtttagccaa 2280
gataatgatt aaaccacggt gtctcttata tgattcaact tttgtttgcc ataagcgta 2340
tcagacgtta ccatggcatt ttgctatgtt ggccaaacaa ttgctcaaac cgatacaatt 2400
gtactttgtc ccgagcaaata ataatcctgc tgacggccca tccaggcaca aacctcctga 2460
ttggacggct tttccataca cccctctctc gaaagcaata tatattccac ataggctatg 2520
tggaacttaa gaattacacc cctctccttc ggagctgctt gccaaaggtat ctttacgtct 2580
acattgctgt tgtcgtgtgt gactgtacct ttggtatgta ccattgttta tgattcttgc 2640
ttatatatgg atatcaatgc ttctagagcc ttagccaatg tgtatgatct accagatgat 2700
ttctttccaa aaatagatga tcttggtaga gatgctaaag acgctttaga gccttattgg 2760
aaatcagatt caataaagaa acatgttttg attgcaactc actttgtgga tctcattgaa 2820
gacttctggc agactacaca gggcatgcat gaaatagccg aatcattaag agctgttata 2880
cctcccacta ctactcctgt tccaccgggt tatcttattc agcacgagga agctgaagag 2940
atacctttgg gagatttatt taaacaccaa gaagaaagga tagtaagttt ccaacccgac 3000
tatccgatta cggctagaat t 3021

```

<210> 6

<211> 984

<212> DNA

<213> duck

<220>

<221> CDS

<222> (1)..(984)

<400> 6

```

atg ggg caa cat cca gca aaa tca atg gac gtc aga cgg ata gaa gga 48
Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly
1 5 10 15

gga gaa ata ctg tta aac caa ctt gcc gga agg atg atc cca aaa ggg 96
Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
20 25 30

act ttg aca tgg tca ggc aag ttt cca aca cta gat cac gtg tta gac 144

```

- 5 -

Thr	Leu	Thr	Trp	Ser	Gly	Lys	Phe	Pro	Thr	Leu	Asp	His	Val	Leu	Asp	
	35						40					45				
cat	gtg	caa	aca	atg	gag	gag	ata	aac	acc	ctc	cag	aat	cag	gga	gct	192
His	Val	Gln	Thr	Met	Glu	Glu	Ile	Asn	Thr	Leu	Gln	Asn	Gln	Gly	Ala	
	50					55				60						
tgg	cct	gct	ggg	gcg	gga	agg	aga	gta	gga	tta	tca	aat	ccg	act	cct	240
Trp	Pro	Ala	Gly	Ala	Gly	Arg	Arg	Val	Gly	Leu	Ser	Asn	Pro	Thr	Pro	
65				70					75					80		
caa	gag	att	cct	cag	ccc	cag	tgg	act	ccc	gag	gaa	gac	caa	aaa	gca	288
Gln	Glu	Ile	Pro	Gln	Pro	Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala	
				85				90						95		
cgc	gaa	gct	ttt	cgc	cgt	tat	caa	gaa	gaa	aga	cca	ccg	gaa	acc	acc	336
Arg	Glu	Ala	Phe	Arg	Arg	Tyr	Gln	Glu	Glu	Arg	Pro	Pro	Glu	Thr	Thr	
			100				105						110			
acc	att	cct	ccg	tct	tcc	cct	cct	cag	tgg	aag	cta	caa	ccc	ggg	gac	384
Thr	Ile	Pro	Pro	Ser	Ser	Pro	Pro	Gln	Trp	Lys	Leu	Gln	Pro	Gly	Asp	
		115				120						125				
gat	cca	ctc	ctg	gga	aat	cag	tct	ctc	ctc	gag	act	cat	ccg	cta	tac	432
Asp	Pro	Leu	Leu	Gly	Asn	Gln	Ser	Leu	Leu	Glu	Thr	His	Pro	Leu	Tyr	
	130					135				140						
cag	tca	gaa	cca	gcg	gtg	cca	gtg	ata	aaa	act	ccc	ccc	ttg	aag	aag	480
Gln	Ser	Glu	Pro	Ala	Val	Pro	Val	Ile	Lys	Thr	Pro	Pro	Leu	Lys	Lys	
145				150					155					160		
aaa	atg	tct	ggt	acc	ttc	ggg	gga	ata	cta	gct	ggc	cta	atc	gga	tta	528
Lys	Met	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	Ala	Gly	Leu	Ile	Gly	Leu	
				165				170						175		
ctg	gta	agc	ttt	ttc	ttg	ttg	ata	aaa	att	cta	gaa	ata	ctg	agg	agg	576
Leu	Val	Ser	Phe	Phe	Leu	Leu	Ile	Lys	Ile	Leu	Glu	Ile	Leu	Arg	Arg	
			180				185						190			
cta	gat	tgg	tgg	tgg	att	tct	ctc	agt	tct	cca	aag	gga	aaa	atg	caa	624
Leu	Asp	Trp	Trp	Trp	Ile	Ser	Leu	Ser	Ser	Pro	Lys	Gly	Lys	Met	Gln	
		195				200						205				
tgc	gct	ttc	caa	gat	act	gga	gcc	caa	atc	tct	cca	cat	tac	gta	gga	672
Cys	Ala	Phe	Gln	Asp	Thr	Gly	Ala	Gln	Ile	Ser	Pro	His	Tyr	Val	Gly	
	210					215					220					
tct	tgc	ccg	tgg	gga	tgc	cca	gga	ttt	ctt	tgg	acc	tat	ctc	agg	ctt	720
Ser	Cys	Pro	Trp	Gly	Cys	Pro	Gly	Phe	Leu	Trp	Thr	Tyr	Leu	Arg	Leu	
225				230						235				240		
ttt	atc	atc	ttc	ctc	tta	atc	ctg	cta	gta	gca	gca	ggc	ttg	ctg	tat	768
Phe	Ile	Ile	Phe	Leu	Leu	Ile	Leu	Leu	Val	Ala	Ala	Gly	Leu	Leu	Tyr	
				245				250						255		
ctg	acg	gac	aac	ggg	tct	act	att	tta	gga	aag	ctc	caa	tgg	gcg	tcg	816
Leu	Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	

- 6 -

260	265	270	
gtc tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg			864
Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro			
275	280	285	
aaa tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act			912
Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr			
290	295	300	
tcc tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg			960
Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr			
305	310	315	320
ctg tct gct ctt ttt tac aag agt			984
Leu Ser Ala Leu Phe Tyr Lys Ser			
325			

<210> 7

<211> 328

<212> PRT

<213> duck

<400> 7

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly	
1	15
Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly	
20	30
Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp	
35	45
His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala	
50	60
Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro	
65	80
Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala	
85	95
Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr	
100	110

- 7 -

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
 115 120 125

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
 130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
 145 150 155 160

Lys Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu
 165 170 175

Leu Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg
 180 185 190

Leu Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln
 195 200 205

Cys Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly
 210 215 220

Ser Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu
 225 230 235 240

Phe Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr
 245 250 255

Leu Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser
 260 265 270

Val Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro
 275 280 285

Lys Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr
 290 295 300

Ser Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr
 305 310 315 320

Leu Ser Ala Leu Phe Tyr Lys Ser
 325

- 8 -

<210> 8

<211> 501

<212> DNA

<213> duck

<220>

<221> CDS

<222> (1)..(501)

<400> 8

atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg	48
Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu	
1 5 10 15	
gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta	96
Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu	
20 25 30	
gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc	144
Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys	
35 40 45	
gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct	192
Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser	
50 55 60	
tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt	240
Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe	
65 70 75 80	
atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg	288
Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu	
85 90 95	
acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc	336
Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val	
100 105 110	
tca gcc ctt ttc tcc tcc atc tct tca cta ctg ccc tcg gat ccg aaa	384
Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys	
115 120 125	
tct ctc gtc gct tta acg ttt gga ctt tca ctt ata tgg atg act tcc	432
Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser	
130 135 140	
tcc tct gcc acc caa acg ctc gtc acc tta acg caa tta gcc acg ctg	480

- 9 -

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu
 145 150 155 160

tct gct ctt ttt tac aag agt
 Ser Ala Leu Phe Tyr Lys Ser
 165

501

<210> 9

<211> 167

<212> PRT

<213> duck

<400> 9

Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu
 1 5 10 15

Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu
 20 25 30

Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys
 35 40 45

Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser
 50 55 60

Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe
 65 70 75 80

Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu
 85 90 95

Thr Asp Asn Gly Ser Thr Ile Leu Gly Lys Leu Gln Trp Ala Ser Val
 100 105 110

Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys
 115 120 125

Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser
 130 135 140

Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu

- 10 -

145

150

155

160

Ser Ala Leu Phe Tyr Lys Ser
165

<210> 10

<211> 483

<212> DNA

<213> duck

<220>

<221> CDS

<222> (1)..(483)

<400> 10

atg	ggg	caa	cat	cca	gca	aaa	tca	atg	gac	gtc	aga	cgg	ata	gaa	gga	48
Met	Gly	Gln	His	Pro	Ala	Lys	Ser	Met	Asp	Val	Arg	Arg	Ile	Glu	Gly	
1				5					10					15		

gga	gaa	ata	ctg	tta	aac	caa	ctt	gcc	gga	agg	atg	atc	cca	aaa	ggg	96
Gly	Glu	Ile	Leu	Leu	Asn	Gln	Leu	Ala	Gly	Arg	Met	Ile	Pro	Lys	Gly	
			20					25					30			

act	ttg	aca	tgg	tca	ggc	aag	ttt	cca	aca	cta	gat	cac	gtg	tta	gac	144
Thr	Leu	Thr	Trp	Ser	Gly	Lys	Phe	Pro	Thr	Leu	Asp	His	Val	Leu	Asp	
		35					40					45				

cat	gtg	caa	aca	atg	gag	gag	ata	aac	acc	ctc	cag	aat	cag	gga	gct	192
His	Val	Gln	Thr	Met	Glu	Glu	Ile	Asn	Thr	Leu	Gln	Asn	Gln	Gly	Ala	
	50					55					60					

tgg	cct	gct	ggg	gcg	gga	agg	aga	gta	gga	tta	tca	aat	ccg	act	cct	240
Trp	Pro	Ala	Gly	Ala	Gly	Arg	Arg	Val	Gly	Leu	Ser	Asn	Pro	Thr	Pro	
65				70					75					80		

caa	gag	att	cct	cag	ccc	cag	tgg	act	ccc	gag	gaa	gac	caa	aaa	gca	288
Gln	Glu	Ile	Pro	Gln	Pro	Gln	Trp	Thr	Pro	Glu	Glu	Asp	Gln	Lys	Ala	
			85					90						95		

cgc	gaa	gct	ttt	cgc	cgt	tat	caa	gaa	gaa	aga	cca	ccg	gaa	acc	acc	336
Arg	Glu	Ala	Phe	Arg	Arg	Tyr	Gln	Glu	Glu	Arg	Pro	Pro	Glu	Thr	Thr	
			100				105						110			

acc	att	cct	ccg	tct	tcc	cct	cct	cag	tgg	aag	cta	caa	ccc	ggg	gac	384
Thr	Ile	Pro	Pro	Ser	Ser	Pro	Pro	Gln	Trp	Lys	Leu	Gln	Pro	Gly	Asp	
		115					120					125				

- 11 -

gat cca ctc ctg gga aat cag tct ctc ctc gag act cat ccg cta tac 432
 Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
 130 135 140

cag tca gaa cca gcg gtg cca gtg ata aaa act ccc ccc ttg aag aag 480
 Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
 145 150 155 160

aaa 483
 Lys

<210> 11

<211> 161

<212> PRT

<213> duck

<400> 11

Met Gly Gln His Pro Ala Lys Ser Met Asp Val Arg Arg Ile Glu Gly
 1 5 10 15

Gly Glu Ile Leu Leu Asn Gln Leu Ala Gly Arg Met Ile Pro Lys Gly
 20 25 30

Thr Leu Thr Trp Ser Gly Lys Phe Pro Thr Leu Asp His Val Leu Asp
 35 40 45

His Val Gln Thr Met Glu Glu Ile Asn Thr Leu Gln Asn Gln Gly Ala
 50 55 60

Trp Pro Ala Gly Ala Gly Arg Arg Val Gly Leu Ser Asn Pro Thr Pro
 65 70 75 80

Gln Glu Ile Pro Gln Pro Gln Trp Thr Pro Glu Glu Asp Gln Lys Ala
 85 90 95

Arg Glu Ala Phe Arg Arg Tyr Gln Glu Glu Arg Pro Pro Glu Thr Thr
 100 105 110

Thr Ile Pro Pro Ser Ser Pro Pro Gln Trp Lys Leu Gln Pro Gly Asp
 115 120 125

- 12 -

Asp Pro Leu Leu Gly Asn Gln Ser Leu Leu Glu Thr His Pro Leu Tyr
 130 135 140

Gln Ser Glu Pro Ala Val Pro Val Ile Lys Thr Pro Pro Leu Lys Lys
 145 150 155 160

Lys

<210> 12

<211> 501

<212> DNA

<213> duck

<220>

<221> CDS

<222> (1)..(501)

<400> 12

atg tct ggt acc ttc ggg gga ata cta gct ggc cta atc gga tta ctg 48
 Met Ser Gly Thr Phe Gly Gly Ile Leu Ala Gly Leu Ile Gly Leu Leu
 1 5 10 15

gta agc ttt ttc ttg ttg ata aaa att cta gaa ata ctg agg agg cta 96
 Val Ser Phe Phe Leu Leu Ile Lys Ile Leu Glu Ile Leu Arg Arg Leu
 20 25 30

gat tgg tgg tgg att tct ctc agt tct cca aag gga aaa atg caa tgc 144
 Asp Trp Trp Trp Ile Ser Leu Ser Ser Pro Lys Gly Lys Met Gln Cys
 35 40 45

gct ttc caa gat act gga gcc caa atc tct cca cat tac gta gga tct 192
 Ala Phe Gln Asp Thr Gly Ala Gln Ile Ser Pro His Tyr Val Gly Ser
 50 55 60

tgc ccg tgg gga tgc cca gga ttt ctt tgg acc tat ctc agg ctt ttt 240
 Cys Pro Trp Gly Cys Pro Gly Phe Leu Trp Thr Tyr Leu Arg Leu Phe
 65 70 75 80

atc atc ttc ctc tta atc ctg cta gta gca gca ggc ttg ctg tat ctg 288
 Ile Ile Phe Leu Leu Ile Leu Leu Val Ala Ala Gly Leu Leu Tyr Leu
 85 90 95

acg gac aac ggg tct act att tta gga aag ctc caa tgg gcg tcg gtc 336

- 13 -

Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	Val		
			100					105					110				
tca	gcc	ctt	ttc	tcc	tcc	atc	tct	tca	cta	ctg	ccc	tcg	gat	ccg	aaa		384
Ser	Ala	Leu	Phe	Ser	Ser	Ile	Ser	Ser	Leu	Leu	Pro	Ser	Asp	Pro	Lys		
		115					120				125						
tct	ctc	gtc	gct	tta	acg	ttt	gga	ctt	tca	ctt	ata	tgg	atg	act	tcc		432
Ser	Leu	Val	Ala	Leu	Thr	Phe	Gly	Leu	Ser	Leu	Ile	Trp	Met	Thr	Ser		
		130				135					140						
tcc	tct	gcc	acc	caa	acg	ctc	gtc	acc	tta	acg	caa	tta	gcc	acg	ctg		480
Ser	Ser	Ala	Thr	Gln	Thr	Leu	Val	Thr	Leu	Thr	Gln	Leu	Ala	Thr	Leu		
145					150				155						160		
tct	gct	ctt	ttt	tac	aag	agt											501
Ser	Ala	Leu	Phe	Tyr	Lys	Ser											
				165													

<210> 13

<211> 167

<212> PRT

<213> duck

<400> 13

Met	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	Ala	Gly	Leu	Ile	Gly	Leu	Leu		
1				5					10					15			

Val	Ser	Phe	Phe	Leu	Leu	Ile	Lys	Ile	Leu	Glu	Ile	Leu	Arg	Arg	Leu		
			20				25						30				

Asp	Trp	Trp	Trp	Ile	Ser	Leu	Ser	Ser	Pro	Lys	Gly	Lys	Met	Gln	Cys		
		35					40					45					

Ala	Phe	Gln	Asp	Thr	Gly	Ala	Gln	Ile	Ser	Pro	His	Tyr	Val	Gly	Ser		
	50					55					60						

Cys	Pro	Trp	Gly	Cys	Pro	Gly	Phe	Leu	Trp	Thr	Tyr	Leu	Arg	Leu	Phe		
65					70					75					80		

Ile	Ile	Phe	Leu	Leu	Ile	Leu	Leu	Val	Ala	Ala	Gly	Leu	Leu	Tyr	Leu		
				85					90					95			

Thr	Asp	Asn	Gly	Ser	Thr	Ile	Leu	Gly	Lys	Leu	Gln	Trp	Ala	Ser	Val		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

- 14 -

100	105	110
Ser Ala Leu Phe Ser Ser Ile Ser Ser Leu Leu Pro Ser Asp Pro Lys 115 120 125		
Ser Leu Val Ala Leu Thr Phe Gly Leu Ser Leu Ile Trp Met Thr Ser 130 135 140		
Ser Ser Ala Thr Gln Thr Leu Val Thr Leu Thr Gln Leu Ala Thr Leu 145 150 155 160		
Ser Ala Leu Phe Tyr Lys Ser 165		